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FIGURE 258

MRGSVECTWGWGHCAPSPLLLWTLTLLFAAPFGLLGKTRQVSLEVIPNWLGPLQNLLHIRAVG
TNSTLHYVWSSLGPLAVVMVATNTPHSTLSINWSLLLSPEPDGGLMVLPKDSIQFSSALVFTR
LLEFDSTNVSDTAAPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGHMNDPTRTFANGS
LAFRVQAFSRSSRPAQPPRLHTADTCQLEVALIGASPRGNRSLFGLEVATLGQGPDCPSMQE
QHSIDDEYAPAVFQLDQLLWGSLSGFAQWRPVAYSQKFGGRESALPCQASPLHPALAYSLPQ
SPIVRAFFGSQNNFCAFNLTFGASTGPGYWDQHYLSWSMLLGVGFPVVDGLSPLVLGIMAVAL
GAPGLMLLGGGLVLLLHHKKYSEYQSIN

Important features:**Signal peptide:**

amino acids 1-35

Transmembrane domain:

amino acids 365-386

N-glycosylation sites:

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234, 333-337

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 397-401

N-myristoylation sites:

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

Leucine zipper pattern:

amino acids 371-393

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FIGURE 259

CAGGCGGGCCCCCGCGCGGCAGGGCCCTGGACCCGCGCGGCTCCCGGGGATGGTGAGCAAGGCGCTGCTGCGCCT
CGTGTCTGCCGTCAACCGCAGGAGGATGAAGCTGCTGCTGGGCATCGCCCTTGCTGGCCTACGTGCGCTCTGTTTG
GGGCAACTTCGTAAATATGAGGTCTATCCAGGAAAATGGTGAACATAAAATTGAAAGCAAGATTGAAGAGATGGT
TGAACCACTAAGAGAGAAAAATCAGAGATTTAGAAAAAGCTTTACCCAGAAATACCCACCAGTAAAGTTTTTATC
AGAAAAGGATCGGAAAAGAATTTTGATAACAGGAGGCGCAGGGTTCGTGGGCTCCCATCTAACTGACAAACTCAT
GATGGACGGCCACGAGGTGACCGTGGTGGACAAFTTCTTTCACGGGCAGGAAGAGAAACGTGGAGCACTGGATCGG
ACATGAGAACTTCGAGTTGATTAAACCACGACGTGGTGGAGCCCCCTCTACATCGAGGTTGACCAGATATACCATCT
GGCATCTCCAGCCTCCCCCTCCAACTACATGTATAATCCTATCAAGACATTAAAGACCAATACGATTGGGACATT
AAACATGTTGGGCTGGCAAAACGAGTCCGTGCCCGTCTGCTCCTGGCCTCCACATCGGAGGTGTATGGAGATCC
TGAAGTCCACCCCTCAAAGTGAGGATTACTGGGGCCACGTGAATCCAATAGGACCTCGGGCCTGCTACGATGAAGG
CAAACGTGTTGCAGAGACCATGTGCTATGCCTACATGAAGCAGGAAGGCGTGGAAGTGCGAGTGGCCAGAATCTT
CAACACCTTTGGGCCACGCATGCACATGAACGATGGGCGAGTAGTCAGCAACTTCATCCTGCAGGCGCTCCAGGG
GGAGCCACTCACGGTATACGGATCCGGGTCTCAGACAAGGGCGTTCAGTACGTCAGCGATCTAGTGAATGGCCT
CGTGGCTCTCATGAACAGCAACGTGACGAGCCCGGTCAACCTGGGGAACCCAGAAGAACACACAATCCTAGAATT
TGCTCAGTTAATTAAAAACCTTGTTGGTAGCGGAAGTGAAATTCAGTTTCTCTCCGAAGCCCAGGATGACCCACA
GAAAAGAAAACCAGACATCAAAAAAGCAAAGCTGATGCTGGGGTGGGAGCCCGTGGTCCCGCTGGAGGAAGGTTT
AAACAAAGCAATTCACACTTCCGTAAAGAACTCGAGTACCAGGCAAATAATCAGTACATCCCCAAACCAAAGCC
TGCCAGAATAAAGAAAGGACGGACTCGCCACAGCTTGAACTCCTCACTTTTAGGACACAAGACTACCATTTGTACAC
TTGATGGGATGTATTTTGGCTTTTGTGTTGTTAAAGAAAGACTTTAACAGGTGTCATGAAGAACAAC
TGGAATTTCACTCTGAAGCTTGCTTTAATGAAATGGATGTGCCTAAAAGCTCCCTCAAAAACTGCAGATTTTG
CCTTGCACTTTTGAATCTCTCTTTTATGTAAAATAGCGTAGATGCATCTCTGCGTATTTTCAAGTTTTTTAT
CTTGCTGTGAGAGCATATGTTGTGACTGTCGTTGACAGTTTTATTTACTGGTTTCTTTGTGAAGCTGAAAAGGAA
CATTAAAGCGGGACAAAAAATGCCGATTTTATTTATAAAAGTGGGTACTTAATAAATGAGTCGTTATACTATGCAT
AAAGAAAAATCCTAGCAGTATTGTCAGGTGCTGGTGGCGCCGGCATTGATTTTAGGGCAGATAAAAGAATTCTGTG
TGAGAGCTTTATGTTTCTCTTTTAAATTCAGAGTTTTTCCAAGGTCTACTTTTGAGTTGCAACTTGACTTTGAAA
TATTCCTGTTGGTCATGATCAAGGATATTTGAAATCACTACTGTGTTTGGCTGCGTATCTGGGGCGGGGGCAGGT
TGGGGGGCACAAAGTTAACATATTCTTGGTTAACCATGGTTAAATATGCTATTTTAAATAAATATTGAAACTCA

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FIGURE 260

MVSKALLRLVSAVNRRRMKLLLGIALLAYVASVWGNFVNMRSIQENGELKIESKIEEMVEPLR
EKIRDLEKSFTQKYPPVKFLSEKDRKRILITGGAGFVGSHLTDKLMMDGHEVTVVDNFFTGRK
RNVEHWIGHENFELINHADVVEPLYIEVDQIYHLASPASPPNYMYPNPIKTLKTNLTIGTLNMLGL
AKRVGARLLLASTSEVYGDPEVHPQSEDIWGHVNPFGPRACYDEGKRVAETMCYAYMKQEGVE
VRVARIFNTFGPRMHMNDGRVVSNFILQALQGEPLTVYGGSGQTRAFQYVSDLVNLGLVALMNS
NVSSPVNLGNPEEHTILEFAQLIKNLVGGSGSEIQFLSEAQDDPQKRKPDIKKAKMLGWEPVV
PLEEGLNKAIHYFRKELEYQANNQYIPKPKPARIKKGRTRHS

Important features:**Signal peptide:**

amino acids 1-32

N-glycosylation site:

amino acids 316-320

Tyrosine kinase phosphorylation site:

amino acids 235-244

N-myristoylation sites:

amino acids 35-41,101-107,383-389

Amidation sites:

amino acids 123-127,233-237

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FIGURE 261

GCGTGGTGC GGGGGCGTGGGGAAATCGGGTTGCCCCAGCCGTTACTGGTCCGCGCAGTCAGGG
CATCCTCCGCATCCTCCACATCCTTCC**ATG**GCTCTGAAGAATAAATTCAGTTGTTTATGGATC
TTGGGTCTGTGTTTGGTAGCCACTACATCTTCCAAAATCCCATCCATCACTGACCCACACTTT
ATAGACAAC TGCATAGAAGCCCAACAACGAATGGCGTGGCAAAGTCAACCCTCCCGCGGCCGAC
ATGAAATACATGATTTGGGATAAAGGTTTAGCAAAGATGGCTAAAGCATGGGCAAACCAAGTGC
AAATTTGAACATAATGACTGTTTGGATAAATCATATAAATGCTATGCAGCTTTTGAATATGTT
GGAGAAAATATCTGGTTAGGTGGAATAAAGTCATTACACCAAGACATGCCATTACGGCTTGG
TATAATGAAACCCAATTTTATGATTTTGATAGTCTATCATGCTCCAGAGTCTGTGGCCATTAT
ACACAGTTAGTTTGGGCCAATTCATTTTATGTCGGTTGTGCAGTTGCAATGTGTCCTAACCTT
GGGGGAGCTTCAACTGCAATATTTGTATGCAACTACGGACCTGCAGGAAATTTTGCAAATATG
CCTCCTTACGCAAGAGGAGAATCTTGCTCTCTCTGCTCAAAAGAAGAGAAATGTGTAAAGAAC
CTCTGCAGGACTCCACAACCTTATTATACCTAACC AAAATCCATTTCTGAAGCCAACGGGGAGA
GCACCTCAGCAGACAGCCTTTAATCCATTCAGCTTAGGTTTTCTTCTTCTGAGAATCTTT**TAA**
TGTCATTTATATACAAAAGAAATTCTCAAATGTTAAAATAAAGGAATAGTTTATTGCTTAATA

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FIGURE 262

MALKNKFSCSLWILGLCLVATTSSKIP SITDPHFIDNCIEAHNEWRGKVNPPAADMKYMIWDKG
LAKMAKAWANQCKFEHNDCLDKSYKCYAAFEYVGENIWLGGIKSFTPRHAITAWYNETQFYDF
DSLSCSRVCGHYTQLVWANSFYVGCAVAMCPNLGGASTAIFVCNYGPAGNFANMPPYARGESC
SLCSKEEKCVKNLCRTPQLIIPNQNPFLKPTGRAPQQTAFNPFSLGFLLLRIF

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation site:

amino acids 119-123

N-myristoylation sites:

amino acids 103-109,150-156,160-166,161-167,175-181

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1:

amino acids 136-156

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2:

amino acids 166-178

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FIGURE 263

CGCCCTCCGACCCGCCCCGCGGCGCATTGTGGGATCTGTGCGGCTTGTCAGGTGGTGGAGGAAA
AGGCGCTCCGTC**ATG**GGGATCCAGACGAGCCCCGTCTGTGCTGGCCTCCCTGGGGGTGGGGCTG
GTCACTCTGCTCGGCCTGGCTGTGGGCTCCTACTTGGTTTCGGAGGTCCCGCCGGCCTCAGGTC
ACTCTCCTGGACCCCAATGAAAAGTACCTGCTACGACTGCTAGACAAGACGACTGTGAGCCAC
AACACCAAGAGGTTCCGCTTTGCCCTGCCACCCGCCACCACACTCTGGGGCTGCCTGTGGGC
AAACATATCTACCTCTCCACCCGAATTGATGGCAGCCTGGTCATCAGGCCATACACTCCTGTC
ACCAGTGATGAGGATCAAGGCTATGTGGATCTTGTCAATCAAGGTCTACCTGAAGGGTGTGCAC
CCCAAATTTCTGAGGGAGGGAAGATGTCTCAGTACCTGGATAGCCTGAAGGTTGGGGATGTG
GTGGAGTTTCGGGGGCCAAGCGGGTTGCTCACTTACACTGGAAAAGGGCATTTTAACATTTCAG
CCCAACAAGAAATCTCCACCAGAACCCCGAGTGGCGAAGAACTGGGAATGATTGCCGGCGGG
ACAGGAATCACCCCAATGCTACAGCTGATCCGGGCCATCCTGAAAGTCCCTGAAGATCCAACC
CAGTGCTTTCTGCTTTTGGCCAACCAGACAGAAAAGGATATCATCTTGCGGGAGGACTTAGAG
GAACTGCAGGCCCGCTATCCCAATCGCTTTAAGCTCTGGTTCCTCTGGATCATCCCCAAAA
GATTGGGCCTACAGCAAGGGCTTTGTGACTGCCGACATGATCCGGGAACACCTGCCCGCTCCA
GGGGATGATGTGCTGGTACTGCTTTGTGGGCCACCCCAATGGTGCAGCTGGCCTGCCATCCC
AACTTGACAAACTGGGCTACTCACAAAAGATGCGATTACCTACT**TG**AGCATCCTCCAGCTTC
CCTGGTGCTGTTTCGCTGCAGTTGTTCCCATCAGTACTCAAGCACTATAAGCCTTAGATTCTT
TTCCTCAGAGTTTCAGGTTTTTTCAGTTACATCTAGAGCTGAAATCTGGATAGTACCTGCAGG
AACAATATTCCTGTAGCCATGGAAGAGGGCAAGGCTCAGTCACTCCTTGGATGGCCTCCTAAA
TCTCCCCGTGGCAACAGGTCCAGGAGAGGGCCCATGGAGCAGTCTCTTCCATGGAGTAAGAAGG
AAGGGAGCATGTACGCTTGGTCCAAGATTGGCTAGTTCCTTGATAGCATCTTACTCTCACCTT
CTTTGTGTCTGTGATGAAAGGAACAGTCTGTGCAATGGGTTTTACTTAAACTTCACTGTTCAA
CCTATGAGCAAATCTGTATGTGTGAGTATAAGTTGAGCATAGCATACTTCCAGAGGTGGTNTT
ATGGAGATGGCAAGAAAGGAGGAAATGATTTCTTCAGATNTCAAAGGAGTCTGAAATATCATA
TTTCTGTGTGTGTCTCTCTCAGCCCCGTGCCAGGCTAGAGGGAAACAGCTACTGATAATCGAA
AACTGCTGTTTGTGGCANGAACCCCTGGCTGTGCAAATAAATGGGGCTGAGGCCCTGTGTGA
TATTGAAGA

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FIGURE 264

MGIQTSPVLLASLGVGLVTLLGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTR
FRFALEPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQGYVDLVIKVYLKGVHPKFP
EGGKMSQYLDLSKVGDVVEFRGPSGLLTYTGKGHFNIQPNKKSPPPEPRVAKKLGMIAGGTGIT
PMLQLIRAILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFLWFTLDHPPKDWAY
SKGFVTADMIREHLPPAPGDDVLVLLCGPPPMVQLACHPNLCLKGYSQKMRFTY

Important features:**Signal peptide:**

amino acids 1-26

N-glycosylation site:

amino acids 214-218

N-myristoylation sites:

amino acids 22-28, 76-82, 128-134, 180-186

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FIGURE 265

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAGA
ACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTATAG
AATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAACCTGCACCTCGGT
TCTATCGATAATCTCAGCACCCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCCGCCTCAGG
CTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCAATGCC
TCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCCAGGAAC
AGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGACCATCTAC
AGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGATGAGCAGA
AGATACCTCTGCATGGATTTTCAGAGGCAACATTTTTGGATCACACTATTTTCGACCCGGAGAAC
TGCAGGTTC AACACCAGACGCTGGAAAACGGGTACGACGTCTACCACTCTCCTCAGTATCAC
TTCCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACCCACCCCCGTAC
TCCCAGTTCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTCAACACCCCCATACCACGG
CGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCTGAACGTGCTGAAGCCCCGG
GCCCCGATGACCCCGGCCCCGGCCTCCTGTTCACAGGAGCTCCCGAGCGCCGAGGACAACAGC
CCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTTCGAGTGAACACGCACGCTGGGGGA
ACGGGCCCCGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCGCTGG

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FIGURE 266

MLGARLRRLWVCALCSVCSMSVLRAYPNASPLLGSWSGGLIHLYTATARNSYHLQIHKNQGHVDG
APHQTTIYSALMIRSEDAGFVVITGVMSRRYLCMDFERGNI FGSHYFDPENCRFQHQTLENGYDV
YHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRNEIPLIHFNTPIPRRHTRSAEDDSERDF
LNVLKPRARMTPAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGFEGCRPFAKFI

Important features:**Signal peptide:**

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

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FIGURE 267

GGCTGAGGGGAGGCCCGGAGCCTTTCTGGGGCCTGGGGGATCCTCTTGCACTGGTGGGTGGAGAGAAGCGCCTGC
AGCCAACCAGGGTCAGGCTGTGCTCACAGTTTCTCTGGCGGCATGTAAAGGCTCCACAAAGGAGTTGGGAGTTC
AAATGAGGCTGCTGCGGACGGCCTGAGGATGGACCCCAAGCCCTGGACCTGCCGAGCGTGGCACTGAGGCAGCGG
CTGACGCTACTGTGAGGGAAAGAAGGTTGTGAGCAGCCCCGAGGACCCCTGGCCAGCCCTGGCCCCAGCCTCTG
CCGGAGCCCTCTGTGGAGGCAGAGCCAGTGGAGCCCACTGAGGCAGGGCTGCTTGGCAGCCACCGGCCTGCAACT
CAGGAACCCCTCCAGAGGCCATGGACAGGCTGCCCCGCTGACGGCCAGGGTGAAGCATGTGAGGAGCCGCCCGG
AGCCAAGCAGGAGGGAAGAGGCTTTCATAGATTCTATTACAAAGAATAACCACCATTTTGCAAGGACC**ATG**AGG
CCTACTGTGCGTGACATGCTGGTGGCTCGGACTGCTGGCTGCCATGGGAGCTGTTGCAGGCCAGGAGGACGGTTTT
GAGGGCACTGAGGAGGGCTCGCCAAGAGAGTTCAATTACCTAAACAGGTACAAGCGGGCGGGCGAGTCCCAGGAC
AAGTGCACCTACACCTTCATTGTGCCCCAGCAGCGGGTCAAGGGTGCCATCTGCGTCAACTCCAAGGAGCCTGAG
GTGCTTCTGGAGAACCAGTGCATAAGCAGGAGCTAGAGCTGCTCAACAATGAGCTGCTCAAGCAGAAGCGGCAG
ATCGAGACGCTGCAGCAGCTGGTGGAGGTGGACGGCGGCATTGTGAGCGAGGTGAAGCTGCTGCGCAAGGAGAGC
CGCAACATGAACTCGCGGGTCACGCAGCTCTACATGCAGCTCCTGCACGAGATCATCCGCAAGCGGGACAACGCG
TTGGAGCTCTCCAGCTGGAGAACAGGATCCTGAACCAGACAGCCGACATGCTGCAGCTGGCCAGCAAGTACAAG
GAGCTGGAGCACAAGTACCAGCACCTGGCCACACTGGCCCCACAACCAATCAGAGATCATCGCGCAGCTTGAGGAG
CACTGCCAGAGGGTGCCCTCGGCCAGGCCCGTCCCCAGCCACCCCCCGCTGCCCCGCCCCGGGTCTACCAACCA
CCCACCTACAACCGCATCATCAACCAGATCTCTACCAACGAGATCCAGAGTGACCAGAACCTGAAGGTGCTGCCA
CCCCCTCTGCCCACTATGCCCACTCTCACCAGCCTCCCATCTTCCACCGACAAGCCGTGCGGGCCCATGGAGAGAC
TGCCTGCAGGCCCTGGAGGATGGCCACGACACCAGCTCCATCTACCTGGTGAAGCCGGAGAACACCAACCGCCTC
ATGCAGGTGTGGTGGGACAGAGACACGACCCCGGGGGCTGGACCGTCATCCAGAGACGCTGGATGGCTCTGTT
AACTTCTTCAGGAAGTGGGAGACGTACAAGCAAGGCTTTGGGAACATTGACGGCGAATACTGGCTGGGCCTGGAG
AACATTTACTGGCTGACGAACCAAGGCAACTACAACTCCTGGTGACCATGGAGGACTGGTCCGGCCGCAAAGTC
TTTGCAGAATACGCCAGTTTCCGCCTGGAACCTGAGAGCGAGTATTATAAGCTGCGGCTGGGGCGCTACCATGGC
AATGCGGGTGACTCCTTTACATGGCACAACGGCAAGCAGTTTCAACCCCTGGACAGAGATCATGATGTCTACACA
GGAAACTGTGCCCACTACCAGAAGGGAGGCTGGTGGTATAACGCCTGTGCCCACTCCAACCTCAACGGGGTCTGG
TACCGCGGGGGCCATTACCGGAGCCGCTACCAGGACGGAGTCTACTGGGCTGAGTTCCGAGGAGGCTCTTACTCA
CTCAAGAAAGTGGTGATGATGATCCGACCGAACCCCAACACCTTCCAC**TAA**GCCAGCTCCCCCTCCTGACCTCTC
GTGGCCATTGCCAGGAGCCACCCCTGGTCACGCTGGCCACAGCACAAAGAACAACCTCCTCACCAGTTTCATCCTGA
GGCTGGGAGGACCGGGATGCTGGATTCTGTTTTCCGAAGTCACTGCAGCGGATGATGGAACTGAATCGATACGGT
GTTTTCTGTCCCTCCTACTTTCCTTCACACCAGACAGCCCCCTCATGTCTCCAGGACAGGACAGGACTACAGACAA
CTCTTTCTTTAAATAAATTAAGTCTCTACAATAAAAAAAA

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FIGURE 268

MRPLCVTCWWLGLLAAMGAVAGQEDGFEGTEEGSPREFIYLNRYKRAGESQDKCTYTFIVPQQ
RVTGAICVNSKEPEVLLLENRVHKQELELLNNELLKQKRQIETLQQLEVDGGIVSEVKLLRKE
SRNMNSRVTLQLYMQLLHEIIRKRDNALELSQLENRIINQTADMLQLASKYKDLEHKYQHLATL
AHNQSEIIAQLEEHCCQRVPSARVPVQPPPAAPPRVYQPPTYNRIINQISTNEIQSDQNLKVLP
PPLPTMPTLTSLPSSTDKPSGPWRDCLQALEDDGHDTSIIYLVKPENTNRLMQVWCDQRHDPGG
WTVIQRRLDGSVNFFRNWETKYQGFGNIDGEYWLGLENIYWLTNQGNKLLVTMEDWSGRKVF
AEYASFRLEPESEYYKLRLGRYHGNAGDSFTWHNGKQFTTLDRDHDVYTGNCAYQKGGWWYN
ACAHSNLNGVWYRGGHYRSRYQDGVYWAEFRGGSSYSLKKVVMIRPNPNTFH

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation sites:

amino acids 164-168, 192-196

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 124-128

Tyrosine kinase phosphorylation sites:

amino acids 177-184, 385-393, 385-394, 461-468

N-myristoylation sites:amino acids 12-18, 18-24, 22-28, 29-35, 114-120, 341-347, 465-471,
473-479**Amidation site:**

amino acids 373-377

Fibrinogen beta and gamma chains C-terminal domain signature:

amino acids 438-451

Fibrinogen beta and gamma chains C-terminal domain proteins:

amino acids 305-343, 365-402, 411-424, 428-458

Trehalase proteins:

amino acids 275-292

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FIGURE 269

GCCGAGCTGAGCGGATCCTCAC**ATG**ACTGTGATCCGATTCTTTCCAGCGGCTTCTGCAACCAA
GCGGGTCTTACCCCCGCTCCTCCGCGTCTCCAGTCCTCGCACCTGGAACCCCAACGTCCCCGA
GAGTCCCCGAATCCCCGCTCCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGC
AGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTCAGGGCGGACCCGTGCAGTC
CAAGTCGCCGCGCTTTGCGTCCTGGGACGAGATGAATGTCCTGGCGCACGGACTCCTGCAGCT
CGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCTGAGCGCGCTGGAGCGGCG
CCTGAGCGCGTGCGGGTCCGCCTGTCAGGGAACCGAGGGGTCCACCGACCTCCCGTTAGCCCC
TGAGAGCCGGGTGGACCCTGAGGTCTTCACAGCCTGCAGACACAACCTCAAGGCTCAGAACAG
CAGGATCCAGCAACTCTTCCACAAGGTGGCCCAGCAGCAGCGGCACCTGGAGAAGCAGCACCT
GCGAATTCAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCACAAGCACCTAGACCATGAGGT
GGCCAAGCCTGCCCGAAGAAAGAGGCTGCCCGAGATGGCCCAGCCAGTTGACCOGGCTCACAA
TGTCAGCCGCTGCAACCGCTGCCCAGGGATTGCCAGGAGCTGTTCCAGGTTGGGGAGAGGCA
GAGTGGACTATTTGAAATCCAGCCTCAGGGGTCTCCGCCATTTTGGTGAAGTCAAGATGAC
CTCAGATGGAGGCTGGACAGTAATTCAGAGGCGCCACGATGGCTCAGTGGACTTCAACCGGCC
CTGGGAAGCCTACAAGGCGGGGTTTGGGGATCCCCACGGCGAGTTCTGGCTGGGTCTGGAGAA
GGTGCATAGCATCACGGGGGACCGCAACAGCCGCTGGCCGTGCAGCTGCGGGACTGGGATGG
CAACGCCGAGTTGCTGCAGTTCCTCGTGCACCTGGGTGGCGAGGACACGGCCTATAGCCTGCA
GCTCACTGCACCCGTGGCCGGCCAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGT
ACCCTTCTCCACTTGGGACCAGGATCACGACCTCCGCAGGGACAAGAAGTGCGCCAAGAGCCT
CTCTGGAGGCTGGTGGTTTGGCACCTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTC
CATCCACAGCAGCGGCAGAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCCGCTA
CTACCCGCTGCAGGCCACCACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCC**TAG**CG
TCCTGGCTGGGCCTGGTCCCAGGCCACGAAAGACGGTGACTCTTGGCTCTGCCCGAGGATGT
GGCCGTTCCTGCCTGGGCAGGGGCTCCAAGGAGGGGGCCATCTGGAACTTGTGGACAGAGAA
GAAGACCACGACTGGAGAAGCCCCCTTCTGAGTGCAGGGGGGCTGCATGCGTTGCCTCCTGA
GATCGAGGCTGCAGGATATGCTCAGACTCTAGAGGCGTGGACCAAGGGGCATGGAGCTTCACT
CCTTGCTGGCCAGGGAGTTGGGGACTCAGAGGGACCCTTGGGGCCAGCCAGACTGGCCTCAA
TGGCGGACTCAGTCACATTGACTGACGGGGACCAGGGCTTGTGTGGGTGAGAGCGCCCTCAT
GGTGCTGGTGCTGTTGTGTGTAGGTCCCCTGGGGACACAAGCAGGCGCCAATGGTATCTGGGC
GGAGCTCACAGAGTTCTTGGAATAAAAGCAACCTCAGAACAC

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FIGURE 270

MTVIRFFPAASATKRVLPVLRVSSPRTWNPVPESPRIPAPRLPKRMSGAPTAGAALMLCAA
TAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAERTRSQLSALERRLSACGSA
CQGTEGSTDLPLAPESRVDPEVLHSLQTLKAQNSRIQQLFHKVAQQQRHLEKQHLRIQHLS
QFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSRHLHRLPRDCQELFQVGERQSGLFETQ
PQGSPPFLVNCKMTSDGGWTVIQRRHDGSVDENRFEAYKAGFGDPHGEFWLGLEKVHSITGD
RNSRLAVQLRDWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPFSGLSVPFSTWDQ
DHDLRDKNCAKSLSGGWFFGTCSHSNLNGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATT
MLIQPMAAEAAS

Important features:**Signal peptide:**

Amino acids 1-13

Transmembrane domain:

Amino acids 53-70

N-glycosylation site:

Amino acids 224-228

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 46-50;118-122

N-myristoylation sites:

Amino acids 50-56;129-135;341-347;357-363

Fibrinogen beta and gamma chains C-terminal domain signature:

Amino acids 396-409

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FIGURE 271

CGGACGCGTGGGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGGG
AACAAG**ATG**GCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGCTG
CTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCGCTTCGGCTGAAGCATTGTGACTCG
GTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACACACCTAC
CCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTT
GTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTCGCT
GAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTCCTCTAACT
CTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACCTCTTCATGG
ACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCCAGAAATCCAG
TACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAAGCAAAATGTCC
TATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGAGAAAGTGATGGC
TTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACTCTTGTCTCTCGGTG
ATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGCAGTATGTTCCCTCT
GAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAGCTAAACAGATATCCA
GCTTCTTCTCTTGTGGTTGTTAGATCTAAAACTGAAGATCATGAAGAAGCAGGGCCTCTACCT
ACAAAAGTGAATCTTGCTCATTCTGAAATT**TAA**GCATTTTTCTTTTAAAGACAAGTGTAATA
GACATCTAAAATTCCTCCTCATAGAGCTTTTAAATGGTTTCATTGGATATAGGCCTTAAG
AAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

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FIGURE 272

MAAPKGS LWVRTQLGLPPLLLLLTMALAGGSGTASAEAFDSVLGDTASCHRA CQLTYPLHTYPK
EEELYACQRGCR LFSICQFVDDGIDLNR TKLECESACTEAYSQSDEQYACHLGCQNQLPFAEL
RQEQ LMSLMPKMHLLFPLTLVRSFWSDMMDSAQS FITSSWTFYLQADDGKIVIFQSKPEIQYA
PHLEQEPTNLRESSLSKMSY LQMRNSQAHRNFLEDGESDGFLRCLSLNSGWILTTTLVLSVMV
LLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAGPLPTK
VNLAHSEI

Important features:**Signal peptide:**

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site:

amino acids 90-94

N-myristoylation sites:

amino acids 28-34,29-35,31-37,86-92

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FIGURE 273

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCCTGCTGCCCCAACCTCACTCTGTG
CTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACCGA
CCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCACGT
GCAGGTACACGGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGCTCAT
AGTGGAGACGGACACGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAGTACAT
CTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTGCGTGTT
CACGGAGATCGTGCTGGAGAACAACCTATACGGCCTTCCAGAACGCCCGGCACGAGGGCTGGTT
CATGGCCTTCACGCGGCAGGGGCGGCCCCGCCAGGCTTCCCGCAGCCGCCAGAACCAGCGCGA
GGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCACGCCGAGAAGCA
GAAGCAGTTCGAGTTTGTGGGCTCCGCCCCCACC CGCCGACCAAGCGCACACGGCGGCCCCA
GCCCCTCACGTAGCTCTGGGAGGCAGGGGGCAGCAGCCCCCTGGGCGCCTCCCCACCCCTTTCC
CTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCCGAGGGAGGACCC
TGAGGGCCCGGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTGCCCCAGGGGCGGC
TGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACTGAGTGTACCCCTGA
TCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCCCGCTGAAAGGTGAGC
GACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGTCCTCAAAATCTGCTTCTCGGATCT
CCCTCAGTCTGCCCCCAGCCCCCAAACCTCCTCCTGGCTAGACTGTAGGAAGGGACTTTTGTTT
GTTTGTTTGTTCAGGAAAAAGAAAGGGAGAGAGAGGAAAAATAGAGGGTTGTCCACTCCTCA
CATTCACGACCCAGGCCTGCACCCCACCCCCACTCCCAGCCCCGGAATAAAACCATTTTCC
TGC

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FIGURE 274

MGAARLLPNLTLCQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRIS
ATAEDGNKFAPKLIVETDTEGSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTEIVLENN
YTAFQONARHEGWFMATRQGRPRQASRSRQNRQEAHFIRKRLYQGQLPFPNHAEKQKQFEFVGS
APTRRTKRTRRPQPLT

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

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FIGURE 275

TATTTACCATATCAGATTCACATTCAGTCCTCAGCAAAATGAAGGGCTCCATTTTCACTCTGT
TTTTATTCTCTGTCCCTATTTGCCATCTCAGAAGTGCGGAGCAAGGAGTCTGTGAGACTCTGTG
GGCTAGAATACATACGGACAGTCATCTATATCTGTGCTAGCTCCAGGTGGAGAAGGCATCTGG
AGGGGATCCCTCAAGCTCAGCAAGCTGAGACAGGAACTCCTTCCAGCTCCCACATAAACGTG
AGTTTTCTGAGGAAAATCCAGCGCAAAACCTTCCGAAGGTGGATGCCTCAGGGGAAGACCGTC
TTTGGGGTGGACAGATGCCCACTGAAGAGCTTTGGAAGTCAAAGAAGCATTCAGTGATGTCAA
GACAAGATTTACAACTTTGTGTTGCACTGATGGCTGTTCCATGACTGATTTGAGTGCTCTTT
GCTAAGACAAGAGCAAATACCCAATGGGTGGCAGAGCTTTATCACATGTTTAATTACAGTGTT
TACTGCCTGGTAGAACACTAATATTGTGTTATTAAAATGATGCCTTTTGGGTAGGCAAACT
TCTTTTCTAAAAGGTATAGCTGAGCGGTTGAAACCACAGTGATCTCTATTTTCTCCCTTTGCC
AAGGTTAATGAACTGTTCTTTTCAAATTCTACTAATGCTTTGAAATTTCAAATGCTGCGCAA
ATTGCAATAAAAATGCTATAAA

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FIGURE 276

MKGSIFTLFLFSVLFAISEVRSKESVRLCGLEYIRTVIYICASSRWRRHLEGIPQAQQAETGN
SFQLPHKREFSEENPAQNLPKVDASGEDRLWGGQMPTEELWKS KKH SVMSRQDLQTLCTDGC
SMTDLSALC

Important features:

Signal sequence:

amino acids 1-18

cAMP- and cGMP-dependent protein kinase phosphorylation site:

amino acids 107-111

N-myristoylation sites:

amino acids 3-9, 52-58, 96-102, 125-131

Insulin family signature:

amino acids 121-136

Insulin family proteins:

amino acids 28-46

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FIGURE 277

GCAGCTGGTTACTGCATTTCTCCATGTGGCAGACAGAGCAAAGCCACAACGCTTTCTCTGCTGGATTAAAGACGG
CCCACAGACCAGAACTTCCACTATACTACTTAAAAATTACATAGGTGGCTTGTCAAATTCATTTGATTAGTATTGT
AAAAGGAAAAAGAAGTTCCCTTCTTACAGCTTGGATTCAACGGTCCAAAACAAAATGCAGCTGCCATTAAAGTCT
CAGATGAACAAACTTCTACACTGATTTTTTAAATCAAGAATAAGGGCAGCAAGTTTCTGGATTCACTGAATCAAC
AGACACAAAAAGCTGGCAATATAGCAACTATGAAGAGAAAAAGCTACTAATAAAATTAACCAACGCATAGAAGAC
TTTTTTTTCTCTTCTAAAAACAACCTAAGTAAAGACTTAAATTTAAACACATCATTTTACAACCTCATTTCAAAA
GAAGACTTTTACCTGGACCTAGGTGTGCTATTCTTCCCTACTAGTGGACACTGGACATTGCAGAGGTGGACAATT
CAAAATTAaaaaaATAAACAGAGAAGATACCCCTCGTGGCCACAGATGGTAAAGAGGAAGCAAAGAAATGTGCATA
CACATTCCTGGTACCTGAACAAAGAATAACAGGGCCAAATCTGTGTCAACACCAAGGGGCAAGATGCAAGTACCAT
TAAAGCATGATCACCAGGATGGACCTTGAAAACCTGAAGGATGTGCTCTCCAGGCAGAAGCGGGAGATAGATGT
TCTGCAACTGGTGGTGGATGTAGATGGAAACATTGTGAATGAGGTAAAGCTGCTGAGAAAGGAAAGCCGTAACAT
GAACTCTCGTGTACTCAACTCTATATGCAATTATTACATGAGATTATCCGTAAGAGGGATAATTCACCTGAACT
TTCCCAACTGGAAAACAAAATCCTCAATGTCAACACAGAAATGTTGAAGATGGCAACAAGATACAGGGAACTAGA
GGTGAATACGCTTCCCTTGACTGATCTTGTCAATAACCAATCTGTGATGATCACTTTGTTGGAAGAACAGTGCTT
GAGGATATTTTCCCGACAAGACACCCATGTGTCTCCCCACTTGTCCAGGTGGTGGCCACAACATATTCCTAACAG
CCAACAGTATACTCCTGGTCTGCTGGGAGGTAACGAGATTCAGAGGGATCCAGGTTATCCCAGAGATTTAATGCC
ACCACCTGATCTGGCAACTTCTCCCACCAAAAGCCCTTTCAGATACCACCGGTAACCTTTCATCAATGAAGGACC
ATTCAAAGACTGTCAGCAAGCAAAGAAGCTGGGCATTCGGTCACTGGGATTTATATGATTAAACCTGAAAACAG
CAATGGACCAATGCAGTTATGGTGTGAAAACAGTTTGGACCCCTGGGGGTGGACTGTTATTCAGAAAAGAACAGA
CGGCTCTGTCAACTTCTTCAGAAATTGGGAAAATTATAAGAAAGGGTTTGGAAACATTGACGGAGAATACTGGCT
TGGACTGGAAAATATCTATATGCTTAGCAATCAAGATAATTACAAGTTATTGATTGAATTAGAAGACTGGAGTGA
TAAAAAAGTCTATGCAGAATACAGCAGCTTTCGTCTGGAACCTGAAAGTGAATTCTATAGACTGCGCCTGGGAAC
TTACCAGGGAAATGCAGGGGATTCATGATGTGGCATAATGGTAAACAATTCACCACACTGGACAGAGATAAAGA
TATGTATGCAGGAAACTGCGCCCACTTTCATAAAGGAGGCTGGTGGTACAATGCCTGTGCACATTCCTAACCTAAA
TGGAGTATGGTACAGAGGAGGCCATTACAGAAGCAAGCACCAAGATGGAAATTTCTGGGCCGAATACAGAGGCGG
GTCATACTCCTTAAGAGCAGTTCAGATGATGATCAAGCCTATTGACTGAAGAGAGACACTCGCCAATTTAAATGA
CACAGAACTTTGACTTTTTCAGCTCTTAAAAATGTAAATGTTACATGTATATTACTTGGCACAATTTATTTCTAC
ACAGAAAGTTTTTAAATGAATTTTACCGTAACTATAAAAGGGAACCTATAAATGTAGTTTCATCTGTCTGCTCAAT
TACTGCAGAAAATTATGTGTATCCACAACCTAGTTATTTTAAAAATTTATGTTGACTAAATACAAAGTTTGTTC
TAAATGTAAATATTTGCCACAATGTAAAGCAAATCTTAGCTATATTTTAAATCATAAATAACATGTTCAAGATA
CTTAACAATTTATTTAAATCTAAGATTGCTCTAACCTCTAGTGAAAAAATATTTTTTAAATTTTCAGCCAAATA
ATGCATTTTATTTTATAAAAATACAGACAGAAAATTAGGGAGAACTTCTAGTTTTGCCAATAGAAAATGTTCTT
CCATTGAATAAAAGTTATTTCAAATGAATTTGTGCCCTTCACACGTAATGATTAAATCTGAATTCCTAATAATA
TATCCTATGCTGATTTTCCCAAAACATGACCCATAGTATTAATACATATCATTTTAAAAAATAAAAAAAACCC
AAAAATAATGCATGCATAATTTAAATGGTCAATTTATAAGACAAATCTATGAATGAATTTTTCAGTGTATCTT
CATATGATATGCTGAACACCAAAATCTCCAGAAATGCATTTTATGTAGTTCTAAAATCAGCAAAATATTGGTATT
ACAAAATGCAGAATATTTAGTGTGCTACAGATCTGAATTATAGTTCTAATTTATTACTTTTTTTCTAATTT
ACTGATCTTACTACTACAAAGAAAAAAACCCCAACCCATCTGCAATTCAAATCAGAAAGTTTGGACAGCTTTAC
AAGTATTAGTGCATGCTCAGAACAGGTGGGACTAAAACAACTCAAGGAAGTGTGGCTGTTTTCCCGATACTGA
GAATTCACAGCTCCAGAGCAGAAGCCACAGGGGCATAGCTTAGTCCAACTGCTAATTTCAATTTACAGTGTAT
GTAACGCTTAGTCTCAGAGTGTCTTTAACTCATCTTTGCAATCAACAACCTTACTAGTGACTTTCTGGAACAAT
TCCTTTTCAGGAATACATATTCATGCTTAGAGGTGACCTTGCCCTTAATATATTTGTGAAGTTAAATTTTAAAGA
TAGCTCATGAACTTTTGCTTAAGCAAAAAGAAAACCTCGAATTGAAATGTGTGAGGCAACATATGCATGGGAAT
AGCTTAATGTGAAGATAATCATTTGGACAACCTCAAATCCATCAACATGACCAATGTTTTTCATCTGCCACATCTC
AAATAAAAACCTCTGGTGAACAAATTAACAAAATATCCAAACCTCAAAAAAA

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FIGURE 278

MKTFTWTGLGVLFLLVDTGHCRGGQFKIKKINQRRYPRATDGKEEAKKCAYTELVPEQRITGP
ICVNTKGQDASTIKDMITRMDLENLKDVLRSRQKREIDVLQLVVDVDGNIVNEVKLLRKESRNM
NSRVTQLYMQLLHEIIRKRDNSLELSQLENKILNVTTEMLKMATRYRELEVKYASLTDLVNNQ
SVMITLLEEQCLRIFSRQDTHVSPPLVQVVPQHIPNSQQYTPGILLGGNEIQRDPGYPRDLMPP
PDLATSPTKSPFKIIPPVTFINEGPFKDCQQAKEAGHSVSGIYMIKPENSNGPMQLWCENSLDP
GGWTVIQKRTDGSVNFFRNWENYKKGFGNIDGEYWLGLENIYMLSNQDNYKLLIELEDWSDKK
VYAEYSSFRLEPESEFYRLRLGTYQGNAGDSMMWHNGKQFTTLDRDKDMYAGNCAHFHKGGWW
YNACAHSNLNGVWYRGGHYRSKHQDGI FWA EYRGGSYS LRAVQMMIKPID

Important features:

Signal sequence:

Amino acids 1-23

N-glycosylation sites:

Amino acids 160-164;188-192

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 120-124

Tyrosine kinase phosphorylation sites:

Amino acids 173-180;387-396

N-myristoylation sites:

Amino acids 70-76;110-116;232-238,343-349;400-406;467-473;
475-487

Fibrinogen beta and gamma chains C-terminal domain signature:

Amino acids 440-453

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FIGURE 279

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCCGCGATCCCGGC
CCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCCGCGCGGGAGCCGGACCGCCG
CCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCCGAGTGCGGAGAAGCC
CGGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAGCGGA
GGAGAAGGAGGAGGAGGCGAACCCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGGCGTCG
TGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTCAGAAGAGGCAAGCCCCGCGAGCGCG
AGAAATCCAACGCCTGCAAGTGTGTCAGCAGCCCCAGCAAAGGCAAGACCAGCTGCGACAAAA
ACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAGAAGAAGAC
CAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACCACTTGCAAGC
TGCAGGCGGATGGAACCATTTGATGGCACCAAAGATGAGGACAGCACTTACACTCTGTTTAACC
TCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCTGTACTTGGCAA
TGAACAGTGAGGGATACTTGTACACCTCGGAACTTTTCACACCTGAGTGCAAATTCAAAGAAT
CAGTGTTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAGCAGCAGTCAGGCC
GAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAACCATGTGAAGAAGA
ACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGTACAAGGAGCCATCAC
TGCACGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACCAAGAGCAGAAGTGTCT
CTGGCGTGCTGAACGGAGGCAAATCCATGAGCCACAATGAATCAACGTAGCCAGTGAGGGCAA
AAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAATTCTTCTAGCAGTCCTTCA
CCCAAAGTTCAAATTTGTCAGTGACATTTACCAAACAAACAGGCAGAGTTCACTATTCTATC
TGCCATTAGACCTTCTTATCATCCATACTAAAGC

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FIGURE 280

MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVSFVRVKLFGSKKRRRRRPE
PQLKGIVTKLYSRQGYHLQLQADGTIDGTDKDEDSTYTLFNLI PVGLRVVAIQGVQTKLYLAMN
SEGLYLTSELTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLNKEGEIMKGNHVKKNK
PAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGVLNNGGKSMHNEST

Important Features:**N-glycosylation site:**

Amino acids 242-246

Glycosaminoglycan attachment sites:

Amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site:

Amino acids 93-100

N-myristoylation sites:

Amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop):

Amino acids 231-239

HBGF/FGF family proteins:

Amino acids 78-94, 102-153

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FIGURE 281

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGGA
CTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGGCA
ACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCCCTCCA
TTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCCCTTCCTGACATTGGCAGTGCCCC
AGTAGGGGTGGGATGAGCGAATATTCCCAAAGCTAAAGTCCCACACCCTGTAGATTACAAGAG
TGGATTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGGTGCCTGAAGATATTTAAACCACG
TCTTGGAAATTTAGTGGGTCTTGCTTTGGGATAGGTGAAGTGAGGACAGACACTGGAGAGGA
GGGAAAGGGGACGTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGGAGTACATA
GGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACTGGCTGCTGTGGAGGGG
GGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAGCGAGTCGGGG
CCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCCAGCGCGCTCCGGG
CGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCT**ATG**GCGGCGCTGGCCAGTAGCCTGAT
CCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTGCGCGCAGCGGCGCGT
GTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTGCTGTCCAAGGTGCG
ACTGTGCGGGGGGCGGCCCCGCGCGGCGGACC GCGGCCCCGGAGCCTCAGCTCAAAGGCATCGT
CACCAAACGTGTTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCGACGGAAGCATCCAGGG
CACCCCAGAGGATACCAGCTCCTTCACCCACTTCAACCTGATCCCTGTGGGCCTCCGTGTGGT
CACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGCTGAGGGACTGCTCTACAG
TTCGCCGCATTTACAGCTGAGTGTGCTTTAAGGAGTGTGTCTTTGAGAATTACTACGTCCT
GTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCCTGGTACCTCGGCCTGGACAA
GGAGGGCCAGGTCATGAAGGGAAACCGAGTTAAGAAGACCAAGGCAGCTGCCCACTTTCTGCC
CAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCCACAGTGTCCCCGAGGCCTCCCC
TTCCAGTCCCCCTGCCCCC**TGA**AATGTAGTCCCTGGACTGGAGGTTCCCTGCACTCCCAGTGA
GCCAGCCACCACCACAACCTGT

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FIGURE 282

MAALASSLIRQKREVPFGGSRPVSAQRRVCPRGTSKLCQKQLLILLSKVRLCGGRPARPDRG
PEPQLKGIVTKLFCRQGGFYLAQNPDGSIQGTPEDTSSFTFNLI PVGLRVVTIQSAKLGHYMA
MNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNRVKK
TKAAAHFLPKLLEVAMYQEPSLHSVPEASPSSPPAP

Important features:**Tyrosine kinase phosphorylation site:**

Amino acids 199-207

N-myristoylation sites:

Amino acids 54-60; 89-95; 131-137

HBGF/FGF family signature:

Amino acids 131-155

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FIGURE 283

ATGCCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTGG
GACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACGGC
AACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGGCGC
CAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTTGCAA
ATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCTTCAAC
CTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTGAAAACAGGGTTGTATATAGCC
ATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTTTAAAGAA
TCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGGAATCTGGT
AGAGCCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGAGTAAAGAAA
ACCAAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCGAGAACCATCT
TTGCATGATGTTGGGGAAACGGTCCCGAAGCCTGGGGTGACGCCAAGTAAAAGCACAAGTGCG
TCTGCAATAATGAATGGAGGCAAACCAGTCAACAAGAGTAAGACAACA**TAG**

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FIGURE 284

MAAAIASGLIRQKRQAREQHWD RPSASRRRSSPSKNRGLCNGNLVDIEFSKVRI FGLKKRRLRR
QDPQLKGIVTRLYCRQGYLQMHPDGALDGTKDDSTNSTLENLIPVGLRVVAIQGVKTGLYIA
MNGEGYLYPSELFTECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNRVKK
TKPAAHFLPKPLEVAMYREPSLHDVGETV PKPGVTPSKSTSASAIMNGGKPVNKS KTT

Important features:**N-glycosylation sites:**

Amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site:

Amino acids 199-207

N-myristoylation sites:

Amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins:

Amino acids 104-155, 171-198

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FIGURE 285

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTTCAGGTCCAGGTTTTGCTTTGA
TCCTTTTCAAAAAGTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACTACCCCT
GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTCAGCCTTCCCCTGGCGGTGGTGAAAGAGAC
TCGGGAGTCGCTGCTTCCAAAGTGCCCGCCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGC
TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC
AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG
GAAGTATTCACAGCCCCAAGGTTTCCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG
AGGAAAATGTATGGATACAACCTTACGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT
ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAACCTATATTAGGGCGCTGGTGTGGTTCTGGTACTGTACCAG
GAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCAAGGCT
TCTGCATCCACTACAACATTGTTCATGCCACATTCACAGAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTT
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAG
AGAGATGCCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTCTTTGGAA
GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCT
CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTG
GTGGGAAGTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC
ACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTGAGGGATTCACAAATCACTCACCGACGTGGCCCTGGAGC
ACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCAGCTCTTGCCCA
GAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTCT
TCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA
ACAGCTCTTTTGAGAGGAGGCCCTAAAGGACAGGAGAAAAGGCTTCAATCGTGGAAAGAAAATTAATGTTGTAT
TAAATAGATCACCAAGCTAGTTTCAGAGTTACCATGTACGTATTCACCTAGCTGGGTTCTGTATTTTCAGTTCTTTC
GATACGGCTTAGGGTAATGTCACTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAAC
TCTAAAGCTCCATGTCTTGGCCCTAAAAATCGTATAAAAATCTGGATTTTTTTTTTTTTTTTTTGTCTCATATTCACAT
ATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACATATGTTGCTATGAATTAACTTGT
GTCATGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAAATTTCTGCCATTTAGAAGAAGAGAACTACA
TTCATGGTTTGGAAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACCTTATCGATAAGTCAGTTTATTTG
TTTCATTGTGTACATTTTTATATCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTAAATATATCT
ATTTTTACCAAAGGTATTTAATATCTTTTTTATGACAACCTTAGATCAACTATTTTTAGCTTGGTAAATTTTTCT
AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTTGTTGCTCTGACAAAATACATGTATTTCA
TTCTCGTATGGTGTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAA
GACTTTTTGAAAATAATTAAATTATCATATCTCCATTCCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGA
AAGTAGACATTAGATCCAGCCATTACTAACCTATTCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT
AAAGCACCTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCGTGTCTGTCTGTGAGTAGGAACACATCCTATTTA
TTGTGATGTTGTGGTTTTATTATCTTAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTTATGTACA
GAAGTATGTCTCTTAACCAGTTCATTTATGTACTCTGGCAATTTAAAGAAAATCAGTAAATATTTTTGCTTGT
AAAATGCTTAATATNGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAATAAAGA
ATGTGGCTATTTTGGGGAGAAAATTAATAAAAAAAAAAAAAAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

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FIGURE 286

MSLFGLLLLTSAAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPRF
PHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWCGS
GTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLLNNA
ITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNNLLTEEVRLYSCTP
RNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP SKVTKKYHEVLQLRPKT
GVRGLHKSLTDVALEHHEECDVCVRGSTGG

Important features:**signal sequence:**

Amino acids 1-14

N-glycosylation sites:

Amino acids 25-29;55-59;254-258

N-myristoylation sites:

Amino acids 15-21;117-123;127-133;281-287;282-288;319-325

Amidation site:

Amino acids 229-233

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FIGURE 287

CAGCGCTGACTGCGCCGCGGAGAAAGCCAGTGGGAACCCAGACCCATAGGAGACCCGCGTCCC
CGCTCGGCCTGGCCAGGCCCGCGCT**ATG**GAGTTCCTCTGGGCCCTCTCTTGGGTCTGTGCT
GCAGTCTGGCCGCTGCTGATCGCCACACCGTCTTCTGGAACAGTTCAAATCCCAAGTTCCGGA
ATGAGGACTACACCATACATGTGCAGCTGAATGACTACGTGGACATCATCTGTCCGCACTATG
AAGATCACTCTGTGGCAGACGCTGCCATGGAGCAGTACATACTGTACCTGGTGGAGCATGAGG
AGTACCAGCTGTGCCAGCCCCAGTCCAAGGACCAAGTCCGCTGGCAGTGCAACCGGCCAGTG
CCAAGCATGGCCCGGAGAAGCTGTCTGAGAAGTTCCAGCGCTTCACACCTTTCACCCTGGGCA
AGGAGTTCAAAGAAGGACACAGCTACTACTACATCTCCAAACCCATCCACCAGCATGAAGACC
GCTGCTTGAGGTTGAAGGTGACTGTGAGTGGCAAATCACTCACAGTCCTCAGGCCCATGACA
ATCCACAGGAGAAGAGACTTGCAGCAGATGACCCAGAGGTGCGGGTTCTACATAGCATCGGTC
ACAGTGCTGCCCCACGCCTCTTCCCAGTTGCCTGGACTGTGCTGCTCCTTCCACTTCTGCTGC
TGCAAACCCCG**TGA**AGGTGTGTGCCACACCTGGCCTTAAAGAGGGACAGGCTGAAGAGAGGGA
CAGGCACTCCAAACCTGTCTTGGGGCCACTTTCAGAGCCCCAGCCCTGGGAACCACTCCCAC
CACAGGCATAAGCTATCACCTAGCAGCCTCAAAACGGGTCAATATTAAGGTTTTCAACCGGAA
GGAGGCCAACCAGCCCGACAGTGCCATCCCCACCTTCACCTCGGAGGGATGGAGAAAGAAGTG
GAGACAGTCCTTTCCACCATTCCTGCCTTTAAGCCAAAGAAACAAGCTGTGCAGGCATGGTC
CCTTAAGGCACAGTGGGAGCTGAGCTGGAAGGGGCCACGTGGATGGGCAAAGCTTGTCAAAGA
TGCCCCCTTCAGGAGAGAGCCAGGATGCCCAGATGAACTGACTGAAGGAAAAGCAAGAAACAG
PTTCTTGCTTGGAAGCCAGGTACAGGAGAGGCAGCATGCTTGGGCTGACCCAGCATCTCCCAG
CAAGACCTCATCTGTGGAGCTGCCACAGAGAAGTTTGTAGCCAGGTAAGTGCATTCTCTCCCAT
CCTGGGGCAGCACTCCCCAGAGCTGTGCCAGCAGGGGGGCTGTGCCAACCTGTTCTTAGAGTG
TAGCTGTAAGGGCAGTGCCCATGTGTACATTCTGCCTAGAGTGTAGCCTAAAGGGCAGGGCCC
ACGTGTATAGTATCTGTATATAAGTTGCTGTGTGTCTGTCCTGATTTCTACAAGTGGAGTTTT
TTTATACAATGTTCTTTGTCTCAAAATAAAGCAATGTGTTTTTTTCGG

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FIGURE 288

MEFLWAPLLGLCCSLAAADRHTVFWNSSNPKFRNEDYTIHVQLNDYVDIICPHYEDHSADAAM
EQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKEFKEGHSYY
YISKPIHQHEDRCLRLKVTVSGKITHSPQAHDNPQEKRLAADDPEVRVLHSIGHSAAPRLFPL
AWTVLLLPLLLLQTP

Important features:**Signal sequence:**

Amino acids 1-17

N-glycosylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 118-127

N-myristoylation site:

Amino acids 10-16

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FIGURE 289

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCTTCTTC
CTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGGGC
CTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCCTCAACCTCCCAGGACCTATCTGGCTC
CAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTGCCGG
GGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAGGTGGA
AACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTGGTAGAG
GTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCTGAGTGAG
GAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGGCCCCGGACCTCTTCCAGTGGCTG
TGCTCAGATTCCCTGAAGCTCTGCTGCCCCGCAGGCACCTTCGGGGCCCTCCTGCCTTCCCTGT
CCTGGGGGAACAGAGAGGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGGGACACGAGGG
GGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCCAGTGTGGCCTT
GGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGTTTTGGCCCCCTGT
GCCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGGCTGGGGCCCTGCAT
CACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACTGTGGAGCTGACCAA
TTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAGGCCTGCCTAGGCTGC
ATGGGGGCAGGGCCAGGTGCTGTAAAGAAGTGTAGCCCTGGCTATCAGCAGGTGGGCTCCAAG
TGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGAACAAAGCAGTGTGAAAAC
ACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAGATGGAAGGCATCTGTGTG
AAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGACAGAAGACGAGTTGGTGGTG
CTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCACGCTGGCTGCTAAGGGCGAC
TTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATGACTGGCTACTGGTTGTCAGAG
CGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATTAATCGCGGCCACCACCTGTAGGA
CCTCCTCCCACCCACGCTGCCCCCAGAGCTTGGGCTGCCCTCCTGCTGGACACTCAGGACAGC
TTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTGCCTTACAGAGCAGCCCAGGTACCC
AGGCCCCGGCAGACAAGGCCCTGGGGTAAAAAGTAGCCCTGAAGGTGGATAACCATGAGCTCT
TCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGAATTTCAAAGTTTTTCTTAATGGTG
GCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTGGTCCTCACAGGGGTGGGGCCATCACAG
CTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGTTCTGTGTTACCCACATCCCCACACCCCA
TTGCCACTTATTTATTCATCTCAGGAAATAAAGAAAGGTCTTGAAAGTTAAAAAAAAAAAAA
AAAAAAAAAAAAA

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FIGURE 290

MAPWPPKGLVPAVLWGLSLFLNLPGPILWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLERT
IRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQQE
APDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAGYGG
EACGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDECGTE
GANCADQFCVNTTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECETEVC
GENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTDELVLVQQMFFGIICAL
ATLAAKGDVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Important features:**Signal sequence:**

Amino acids 1-29

Transmembrane domain:

Amino acids 342-392

N-glycosylation sites:

Amino acids 79-83;205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 290-294

Aspartic acid and asparagine hydroxylation site:

Amino acids 321-333

EGF-like domain cysteine pattern signature:

Amino acids 181-193

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FIGURE 291

CAGGTCCAACTGCACCTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGACCCAC
GCGTCCGAACACAGGTCTTGTGCTGCAGAGAAGCAGTTGTTTTGCTGGAAGGAGGGAGTGCGCGGGCTGCCCC
GGGCTCCTCCCTGCCGCCCTCTCTCAGTGGATGGTTCCAGGCACCCCTGTCTGGGGCAGGGAGGGACAGGCCTGC
ACATCGAAGGTGGGGTGGGACCAGGCTGCCCCCTCGCCCCAGCATCCAAGTCTTCCCTTGGGGCGCCCGTGGCCCTG
CAGACTCTCAGGGCTAAGGTCTCTGTGCTTTTTGGTTCCACCTTAGAAGAGGCTCCGCTTGACTAAGAGTAGC
TTGAAGGAGGCACCAATGCAGGAGCTGCATCTGCTCTGGTGGGCGCTTCTCCTGGGCCTGGCTCAGGCCTGCCCTG
AGCCCTGCGACTGTGGGGAAAAGTATGGCTTCCAGATCGCCGACTGTGCCTACCGCGACCTAGAATCCGTGCCGC
CTGGCTTCCCCGGCCAATGTGACTACACTGAGCCTGTGAGCCAACCGGCTGCCAGGCTTGCCGGAGGGTGCCTTCA
GGGAGGTGCCCCTGCTGCAGTCGCTGTGGCTGGCACACAATGAGATCCGCACGGTGGCCGCCGGAGCCCTGGCCT
CTCTGAGCCATCTCAAGAGCCTGGACCTCAGCCACAATCTCATCTCTGACTTTGCCTGGAGCGACCTGCACAACC
TCAGTGGCCTCCAATTGCTCAAGATGGACAGCAACGAGCTGACCTTCATCCCCCGGACGCTTCCGCAGCCTCC
GTGCTCTGCGCTCGCTGCAACTCAACCACAACCGCTTGACACACATTGGCCGAGGGCACCTTCACCCCGCTCACCG
CGCTGTCCACCTGCAGATCAACGAGAACCCCTTCGACTGCACCTGCGGCATCGTGTGGCTCAAGACATGGGCCC
TGACCACGGCCGTGTCCATCCCGAGCAGGACAACATCGCCTGCACCTCACCCCATGTGCTCAAGGSTACACCGC
TGAGCCGCTGCCGCCACTGCCATGCTCGGCGCCCTCAGTGCAGCTCAGCTACCAACCCAGCCAGGATGGTGCCG
AGCTGCGGCCTGGTTTTGTGCTGGCACTGCACTGTGATGTGGACGGGCAGCCGGCCCTCAGCTTCAGTGGCACA
TCCAGATACCCAGTGGCATTGTGGAGATCACCAGCCCCAACGTGGGCACATGATGGGCGTGCCCTGCCTGGCACCC
CTGTGGCCAGCTCCCAGCCGCGCTTCCAGGCCTTTGCCAATGGCAGCCTGCTTATCCCCGACTTTGGCAAGCTGG
AGGAAGGCACCTACAGCTGCCTGGCCACCAATGAGCTGGGCAGTGCTGAGAGCTCAGTGGACGTGGCACTGGCCA
CGCCCGGTGAGGGTGCTGAGGACACACTGGGGCGCAGGTTCCATGGCAAAGCGTTGAGGGAAAGGGCTGCTATA
CGGTTGACAACGAGGTGCAGCCATCAGGGCGGAGGACAATGTGGTCAFCATCTACCTCAGCCGTGCTGGGAACC
CTGAGGCTGCAGTCGCAGAAGGGGTCCCTGGGCAGCTGCCCCCAGGCCTGCTCCTGCTGGGCCAAAGCCTCCTCC
TCTTCTTCTTCTCACCTCCTTCTAGCCCCACCCAGGGCTTCCCTAACTCCTCCCCTTGCCCTACCAATGCCCC
TTTAAGTGCTGCAGGGGTCTGGGGTTGGCAACTCCTGAGGCCTGCATGGGTGACTTCACATTTTCTACCTCTCC
TTCTAATCTCTTCTAGAGCACCTGCTATCCCCAACTTCTAGACCTGCTCCAACTAGTGAAGTAGGATAGAATTTG
ATCCCCCTAACTCACTGTCTGCGGTGCTCATTTGCTGCTAACAGCATTGCCCTGTGCTCTCCTCTCAGGGGCAGCATG
CTAACGGGGCGACGTCTTAATCCAACCTGGGAGAAGCCTCAGTGGTGGAAATCCAGGCACTGTGACTGTCAAGCTG
GCAAGGGCCAGGATTGGGGGAATGGAGCTGGGGCTTAGCTGGGAGGTGGTCTGAAGCAGACAGGGAAATGGGAGAG
GAGGATGGGAAGTAGACAGTGGCTGCTATGGCTCTGAGGCTCCCTGGGGCCTGCTCAAGCTCCTCCTGCTCCTTG
CTGTTTTCTGATGATTTGGGGGCTTGGGAGTCCCTTTGTCTCATCTGAGACTGAAATGTGGGGATCCAGGATGG
CCTTCCTTCTCTTACCCTTCTCCTCCTCAGCCTGCAACCTCTATCCTGGAACCTGTCTCCTTCTCCCCAACT
ATGCATCTGTTGTCTGCTCCTCTGCAAAGGCCAGCCAGCTTGGGAGCAGCAGAGAAATAAACAGCATTCTGATG
CCAAAAAAGGGCGCGCCGCGACTCTAGAGTCGACCT

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FIGURE 292

MQELHLLWWALLLGLAQACPEPCDCGGEKYGFQIADCAYRDLESVPPGFANVTTLSSLNRLP
GLPEGAFFREVPLLQSLWLAHNEIRTVAAAGALASLSHLKSLDLSHNLISDFAWSDLHNLSALQL
LKMDSNELTFIPRDAFRSLRALRSLQLNHNRLHTLAEGTFTPLTALSHLQINENPFDCTCGIV
WLKTWALTAVSIPEQDNIACTSPHVLKGTPLSRLPPLPCSAPSVQLSYQPSQDGAELRPGFV
LALHCDVDGQPAPQLHWHIQIPSGIVEITSPNVGTDGRALPGTPVASSQPRFQAFANGSLLIP
DFGKLEEGTYSCLATNELGSAESSVDVALATPGEGGEDTLGRRFHGKAVEGKGCYTVDNEVQP
SGPEDNVVIIYLSRAGNPEAAVAEGVPGQLPPGLLLLQSLLLFFFLTSF

Important features:**Signal peptide:**

amino acids 1-18

Transmembrane domain:

amino acids 403-418

N-glycosylation sites:

Amino acids 51-55,120-124,309-313

Tyrosine kinase phosphorylation site:

amino acids 319-326

N-myristoylation sites:amino acids 14-20,64-70,92-98,218-224,294-300,323-329,334-340,
350-356,394-400**Amidation site:**

amino acids 355-359

Leucine Rich Repeat:

amino acids 51-74,75-98, 99-122,123-146,147-170

Leucine rich repeat C-terminal domain:

amino acids 180-230

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FIGURE 293

ACTTGGAGCAAGCGGCGGGCGGGGAGACAGAGGCAGAGGCAGAAGCTGGGGCTCCGTCTCGCCTCCACAGAGCG
 ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCTGCC
 TCGCTTCCAGGCGCGGGCGGCTGCAGCCTTGCCCTCTTGCTCGCCTTGAAAATGGAAGATGCTCGCAGGCT
 GCTTTCTGCTGATCCTCGGACAGATCGTCTCTCTCTGCGGAGGCCAGGGAGCGGTCACTGGGAGGTCCATCT
 CTAGGGGCGAGACACGCTCGGACCCACCCGACAGACGGCCCTTCTGGAGAGTTCTGTGAGAACAAAGCGGGCAGACC
 TGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTTCATCGTGGACA
 TCTTGCAATTCTTGGACATTGGTCTGATGTCAACCCGAGTGGGCGCTGCTCCAATATGGCAGCACTGTCAAGAATG
 AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACGG
 GCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCGGCCCTGA
 GGGAGAATGTGCCACGGGTCAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA
 AGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG
 GGAGTGAGCCCCATGAGGACCATGTCTCTTGTGGCCAAATTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC
 AGAAGAAGTTGTGCACGGGCCACATGTGCAGACCCCTGGAGCATAACTGTGCCACTTCTGCATCAACATCCCTG
 GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT
 GTGCCATGGAGGACCACAACTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGTGTACAGTG
 GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCCTCAGAAAACACGGATGTGAAC
 ATGAGTGTGTAAATGCTGATGGCTCCTACCTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAAA
 CGTGCAACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCGTCAACATGGAGGAGAGCT
 ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAACCTGCAGCCGAGTGGACCACTGTGCAC
 AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCTTCTGTCTGCCAGTGTCTAGAAGGCTTCC
 TCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCCCTGCTGAGTGACCATGGTTGTGAATACTCCT
 GTGTCAACATGGACAGATCCTTTGCCCTGTCACTGTCTTGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG
 CAAAATTGGACTCTTGTGCTCTGGGGGACCACGGTGTGTGAACATTCTGTGTGAAGCAGTGAAGATTCTGTTTGTGT
 GCCAGTGCTTTGAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG
 ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACAGTGCAGTGTCTGGAGGGATTCCGGCTCG
 CTGAGGATGGGAACGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACCATGGCTGCCAAGACATTTGTGTGA
 ATAATGGGAATTCTTACATCTGCAAAATGCTCAGAGGGATTGTGTTCTAGCTGAGGACGGAAGACGGTGAAGAAAT
 GCACTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAGAATTTTGAGGTCTG
 TGAAGCAGTTTGTCACTGGAATTATAGATTCTTTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGT
 ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCAACTCAGCCAAAGACATGAAAAAGCCGTGGCCC
 ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAGTTTTACCCAAG
 GAGAAGGGGCCAGGCCCCCTTTCCACAAGGGTGCCAGAGCAGCCATTGTGTTACCGACGGACGGGCTCAGGATG
 ACSTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTGTTGGGGTAGGAAAAGCCATTG
 AGGAGGAACATAAGAGATTGCCTCTGAGCCCAACAAAGCATCTCTTCTATGCCGAAGACTTCAGCACAAATGG
 ATGAGATAAGTGAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAAGACAGGACTCTCCAG
 CAGGGGAACCTGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
 CCTGTTCTAATTTTGCAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT
 CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACACGATCAATGCAATGTGAAAACCTTATAATGT
 TCCAGAACCTTGCAACGAAGAAGTAAGAAAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC
 TGGAAAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTATCACGGATTACAAT
 GAACGCAGTGACAGAGCCCCAAAGCTCAGGCTATTGTAAATCAATAATGTTGTGAAGTAAACAATCAGTACTGA
 GAAACCTGGTTTGGCACAGAACAAAGACAAGAAGTATACACTAATTTGTATAAATTTATCTAGGAAAAAATCCT
 TCAGAATTTCTAAGATGAATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC
 AACTTGTCTCTGCTCATCTGCTTGTGTGCAATCTCATTTGACTATACGATAAAGTTTGCACAGTCTTACTT
 CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTTGTACTGGACTTTACCTTGATATATGTATATGGATGTATG
 CATAAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATT'TTTTATACAATATTAAATTCACCACTTCAG

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FIGURE 294

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPQTALLESSCENKRADLVFIID
SSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAVKR
MRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARDTGI
LIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHNCAHF
CINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYALAEDG
KRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKPGEHECVN
MEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLINEDLKTC
SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTC AKLDSCALGDHGCEHSCVSSD
SFVCQC FEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLAEDGKRCRRK
DVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVIDGSKSLGEENF
EVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVAHMKYMGKGSMT
GLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKANGITMYAVGVGKA
IEEELQEIASPTNKHFLFYAEDFSTMD EISEKLKKGICEALEDS DGRQDSPAGELPKTVQOPT
ESEPV TINIQLLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPLEEKHDQCKCENLIM
FQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Important features:**Signal sequence:**

Amino acids 1-23

N-glycosylation site:

Amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 115-119;606-610;892-896

N-myristoylation sites:

Amino acids 133-139;258-264;299-305;340-346;453-459;494-500;
639-645;690-694;
752-758;792-798

Amidation sites:

Amino acids 314-318;560-564;601-605

Aspartic acid and asparagine hydroxylation sites:

Amino acids 253-265;294-306;335-347;376-388;417-429;
458-470;540-552;581-593

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FIGURE 295

GGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCGCAGCGCTACCCGC
CATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTGCTGCTGCCGCCCGC
GCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCTGGTGGACAAGTTTAA
CCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACACGGCTTGGGAGGAAAA
GACGCTGTCCAAGTACGAGTCCAGCGAGATTCGCCTGCTGGAGATCCTGGAGGGGCTGTGCGA
GAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGAGCACCTGGAGGCCTGGTG
GCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTTGTGTGAAGACACTGAAAGT
GTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGCCAGGGCGGATCCCAGAGGCC
CTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACAGGGCGACGGGTCTTGCCGGTG
CCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGGACGGCTACTTCAGCTCGCTCCG
GAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCTTGCAAGACGTGCTCGGGCCTGAC
CAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCTGGACGAGGGCGCCTGTGTGGATGT
GGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTGCGCAGTTCTGTAGAAGCCCAACGG
CTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTGGGCTGCACAGGGGAAGGGCCAGGAAA
CTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCACGGACAGTGTGCAGATGTGGACGAGTG
CTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACGAAAACCTGCTACAATACTCCAGGGAGCTA
CGTCTGTGTGTGTCCTGACGGCTTCGAAGAAACGGAAGATGCCTGTGTGCCGCCGGCAGAGGC
TGAAGCCACAGAAGGAGAAAGCCCGACACAGCTGCCCTCCCGCGAAGACCTG**TAA**TGTGCCGG
ACTTACCCTTTAAATTATTCAGAAGGATGTCCCGTGGAATGTGGCCCTGAGGATGCCGTCT
CCTGCAGTGGACAGCGCGGGGAGAGGCTGCCTGCTCTTAACGGTTGATTCTCATTTGTCCC
TTAAACAGCTGCATTTCTTGGTTGTTCTTAAACAGACTTGTATATTTTGATACAGTTCTTTGT
AATAAAATTGACCATTGTAGGTAATCAGGAGGAAAAAAAAA

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FIGURE 296

MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVDTAKKNFEGGGNTAWEEK
TL SKYESSEIRLLEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKT LKV
CCSPGTYGPDCLACQGGSQRPCSGNGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLR
NETHSICTACDESKTCSGLTNRDCGECEVGWVLDEGACVDVDECAAEPPPCSAAQFCKNANG
SYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKTCVRKNENCYNTPGSY
VCVCPDGFEETEDACVPPAEAEATEGESPTQLPSREDL

Important features:**Signal peptide:**

Amino acids 1-24

N-glycosylation sites:

Amino acids 190-194;251-255

Glycosaminoglycan attachment sites:

Amino acids 149-153;155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 303-310

N-myristoylation sites:Amino acids 44-50;54-60;55-61;81-87;150-156;158-164;164-170;
252-258;313-319**Aspartic acid and asparagine hydroxylation site:**

Amino acids 308-320

EGF-like domain cysteine pattern signature:

Amino acids 166-178

Leucine zipper pattern:

Amino acids 94-116

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FIGURE 297

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAGAAAGAAGAGGAAG
ATGTTGGGCAACATTTATTTAACATGCTCCACAGCCCGGACCCTGGCATCATGCTGCTATTCCTGCAAATACTGA
AGAAGCATGGGATTTAAATATTTTACTTCTAAATAAATGAATTACTCAATCTCCTATGACCATCTATACATACTC
CACCTTCAAAAAGTACATCAATATTATATCATTAAGGAAATAGTAACCTTCTCTTCTCCAATATGCATGACATTT
TTGGACAATGCAATTGTGGCACTGGCACTTATTTCACTGAAGAAAACTTTGTGGTTCTATGGCATTTCATCATTT
GACAAATGCAAGCATCTTCCTTATCAATCAGCTCCTATTGAACTTACTAGCACTGACTGTGGAATCCTTAAGGGC
CCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACTCCGAATTCATGTGCTACTTGGCCTAGCTA
TCACTACACTAGTACAAGCTGTAGATAAAAAAGTGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTTGGT
TTACACCCAGATCCATTTATATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCTTTTAACTTTCCAGCCA
GATTGCCAGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAGACTTTC
CAGTAAACCTTACTGGCCTGGATTTATCTCAAAACAATTTATCTTCAGTCACCAATATTAATGTAAAAAGATGC
CTCAGCTCCTTTCTGTGTACCTAGAGGAAAACAACTTACTGAACTGCCTGAAAAATGTCTGTCCGAAGTGAAGCA
ACTTACAAGAAGTCTATATTAATCACAACCTTGCTTTCTACAATTTACCTGGAGCCTTTATTTGGCCTACATAATC
TTCTTCGACTTCATCTCAATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAAATCTAG
AGATTCTGATGATTGGGGAAATCCAATTTATCAGAATCAAAGACATGAACTTTAAGCCTCTTATCAATCTTCGCA
GCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCCTTGGTTGGACTGGAAAACCTAGAAAGCA
TCTCTTTTTACGATAACAGGCTTATTAAAGTACCCCATGTTGCTCTTCAAAAAGTTGTAAATCTCAAATTTTTGG
ATCTAAATAAAAATCCTATTAATAGAATACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGA
TAAATAATATGCCTGAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAG
CTACTAACAAACCCTAGATTGTCTTACATTACCCCCAATGCATTTTTCAGACTCCCCAAGCTGGAATCACTCATGC
TGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTTGAGTCTCTGCCAAACCTCAAGGAATCAGCATAC
ACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTGGATGAACATGAACAAAACCAACATTCGATTTCATGGAGC
CAGATTCACTGTTTTGCGTGGACCCACCTGAATTCGAAGGTGAGAAATGTTGGCAAGTGCATTTCAAGGACATGA
TGGAAATTTGTCTCCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGTTT
CCTTTCAGTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTTCTGGTCAAAAACCTCTTGC
CTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACTAGATATAAATGGGTAAGTCCCAAGAAG
GGGGTTTATATACTTGTATAGCAACTAACCTAGTTGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGAT
CTTTTCCACAAGATAACAATGGCTCTTTGAATATTAATAAAGAGATATTCAGGCCAATTCAGTTTTGGTGTCTT
GGAAAGCAAGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCATGCTG
CGCAAAGTGCTCGAATACCATCTGATGTCAAGGTATATAATCTTACTCATCTGAATCCATCAACTGAGTATAAAA
TTTGATTTGATATTTCCACCATCTATCAGAAAAACAGAAAAAATGTGTAAATGTCACCACCAAGGTTTGCACC
CTGATCAAAAAGAGTATGAAAAGAATAATACCACAACACTTATGGCCTGTCTTGGAGGCCTTCTGGGGATTATTG
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